

SEQUENCE LISTING

<110> Lye, Stephen
Dong, Xuesen

<120> METHODS AND COMPOSITIONS FOR MODULATING A STEROID RECEPTOR

<130> MTS6USA

<140> PCT/CA2005/000042
<141> 2005-01-14

<150> 60/536,598
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<170> PatentIn version 3.3

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35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
50 55 60

Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
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Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
85 90 95

Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
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 Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
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 Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
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 Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Ala Val Thr Ser Ala
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 Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
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 Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
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 Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
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 Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
 225 230 235 240
 Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
 245 250 255
 Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
 260 265 270
 Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
 275 280 285
 Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
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 Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
 305 310 315 320
 Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
 325 330 335
 Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
 340 345 350
 Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr

Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Gly Ile
625 630 635 640

Gly Tyr Glu Ala Asn Pro Gly Val Pro Pro Ala Thr Met Ser Gly Ser
645 650 655

Met Met Gly Ser Asp Met Arg Thr Glu Arg Phe Gly Gln Gly Gly Ala
660 665 670

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Pro Arg Phe
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Ser Pro Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly
35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
50 55 60

Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
65 70 75 80

Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
85 90 95

Gln Gln Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
100 105 110

Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Thr Pro Pro Ala Ser
 115 120 125
 Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
 130 135 140
 Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Ala Val Thr Ser Ala
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 Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
 165 170 175
 Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
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 Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
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 Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
 210 215 220
 Ser Thr Pro Gly Gly His Pro Lys Pro Pro Arg Arg Gly Gly Gly Glu
 225 230 235 240
 Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
 245 250 255
 Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
 260 265 270
 Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
 275 280 285
 Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
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 Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
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 Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
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 Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr
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His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
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Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
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Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
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Glu Gly Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu
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Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
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Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Thr Arg Phe
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Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
485 490 495

Leu Asp Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met
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Lys Asp Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His
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Glu His Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu
530 535 540

Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
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Lys Glu Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Arg Glu Glu
565 570 575

Glu Met Met Ile Arg Gln Arg Glu Met Glu Asp Gln Met Arg Arg Gln
580 585 590

Arg Glu Glu Ser Tyr Ser Arg Met Gly Tyr Met Asp Pro Arg Glu Arg
595 600 605

Asp Met Arg Met Gly Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr
610 615 620

Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Ile

Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala
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 Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
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 Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
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 Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
 195 200 205
 Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
 210 215 220
 Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
 225 230 235 240
 Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
 245 250 255
 Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
 260 265 270
 Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
 275 280 285
 Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
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 His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
 370 375 380
 Glu Leu Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala
 385 390 395 400

Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
 405 410 415
 Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
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 Glu Gly Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu
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 Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
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 Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe
 465 470 475 480
 Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
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 Glu His Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu
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 Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
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 Lys Glu Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Arg Glu Glu
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 Asp Met Arg Met Gly Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr
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 Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Ile
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Ser Ser Lys Pro Val Val Ala Gln Gly Pro Gly Pro Ala Pro Gly Val
 35 40 45

Gly Ser Ala Pro Pro Ala Ser Ser Ser Ala Pro Pro Ala Thr Pro Pro
 50 55 60

Thr Ser Gly Ala Pro Pro Gly Ser Gly Pro Gly Pro Thr Pro Thr Pro
 65 70 75 80

Pro Pro Ala Val Thr Ser Ala Pro Pro Gly Ala Pro Pro Pro Thr Pro
 85 90 95

Pro Ser Ser Gly Val Pro Thr Thr Pro Pro Gln Ala Gly Gly Pro Pro
 100 105 110

Pro Pro Pro Ala Ala Val Pro Gly Pro Gly Pro Gly Pro Lys Gln Gly
 115 120 125

Pro Gly Pro Gly Gly Pro Lys Gly Gly Lys Met Pro Gly Gly Pro Lys
 130 135 140

Pro Gly Gly Gly Pro Gly Leu Ser Thr Pro Gly Gly His Pro Lys Pro
 145 150 155 160

Pro His Arg Gly Gly Gly Glu Pro Arg Gly Gly Arg Gln His His Pro
 165 170 175

Pro Tyr His Gln Gln His His Gln Gly Pro Pro Pro Gly Gly Pro Gly
 180 185 190

Gly Arg Ser Glu Glu Lys Ile Ser Asp Ser Glu Gly Phe Lys Ala Asn
 195 200 205

Leu Ser Leu Leu Arg Arg Pro Gly Glu Lys Thr Tyr Thr Gln Arg Cys
 210 215 220
 Arg Leu Phe Val Gly Asn Leu Pro Ala Asp Ile Thr Glu Asp Glu Phe
 225 230 235 240
 Lys Arg Leu Phe Ala Lys Tyr Gly Glu Pro Gly Glu Val Phe Ile Asn
 245 250 255
 Lys Gly Lys Gly Phe Gly Phe Ile Lys Leu Glu Ser Arg Ala Leu Ala
 260 265 270
 Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly Arg Gln
 275 280 285
 Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val Arg Asn
 290 295 300
 Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser Gln
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 Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly Arg
 325 330 335
 Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala Arg
 340 345 350
 Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr Thr Thr
 355 360 365
 Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp Glu Asp
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 Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln Lys Glu
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 Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu Tyr Glu
 405 410 415
 Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln Gln Arg
 420 425 430
 Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu Glu Ser
 435 440 445
 Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu Arg Gln
 450 455 460

Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu His
465 470 475 480

Asn Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln Glu Glu
485 490 495

Glu Arg Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg Glu Met
500 505 510

Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg Met Gly
515 520 525

Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly Gly Ala
530 535 540

Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro Pro
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Leu Gly Gly Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly Val Pro
565 570 575

Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg Thr Glu
580 585 590

Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly Pro Arg
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Tyr Glu Gly Pro Asn Lys Lys Pro Arg Phe
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 35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
 50 55 60

Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
 65 70 75 80

Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
 85 90 95

Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
 100 105 110

Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
 115 120 125

Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
 130 135 140

Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala
 145 150 155 160

Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
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Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
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Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
 195 200 205

Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
 210 215 220

Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
 225 230 235 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
 245 250 255

Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
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Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
 275 280 285

Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu

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Pro 305	Ala Asp Ile Thr Glu 310	Asp Glu Phe Lys Arg 315
	Leu Phe Ala Lys Tyr 320	
Gly Glu Pro Gly	Glu 325	Val Phe Ile Asn Lys 330
	Gly Lys Gly Phe Gly 335	Phe
Ile Lys Leu	Glu 340	Ser Arg Ala Leu Ala 345
	Glu Ile Ala Lys Ala 350	Glu Leu
Asp Asp Thr 355	Pro Met Arg Gly Arg 360	Gln Leu Arg Val Arg 365
	Phe Ala Thr	
His Ala 370	Ala Ala Leu Ser Val 375	Arg Asn Leu Ser Pro 380
	Tyr Val Ser Asn	
Glu 385	Leu Leu Glu Glu Ala 390	Phe Ser Gln Phe Gly 395
	Pro Ile Glu Arg Ala 400	
Val Val Ile Val	Asp 405	Asp Arg Gly Arg Ser 410
	Thr Gly Lys Gly Ile 415	Val
Glu Phe Ala	Ser 420	Lys Pro Ala Ala Arg 425
	Lys Ala Phe Glu Arg 430	Cys Ser
Glu Gly Val 435	Phe Leu Leu Thr Thr 440	Thr Pro Arg Pro Val 445
	Ile Val Glu	
Pro Leu Glu Gln Leu Asp Asp 455	Glu Asp Gly Leu Pro 460	Glu Lys Leu Ala
Gln Lys Asn Pro Met Tyr 470	Gln Lys Glu Arg Glu 475	Thr Pro Pro Arg Phe 480
Ala Gln His Gly Thr 485	Phe Glu Tyr Glu Tyr 490	Ser Gln Arg Trp Lys 495
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Arg Gln Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val
50 55 60

Arg Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe
65 70 75 80

Ser Gln Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg
85 90 95

Gly Arg Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala
100 105 110

Ala Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr
115 120 125

Thr Thr Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp
130 135 140

Glu Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln
145 150 155 160

Lys Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu
165 170 175

Tyr Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln
180 185 190

Gln Arg Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu
195 200 205

Glu Ser Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu
210 215 220

Arg Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu
225 230 235 240

Leu His Asn Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln
245 250 255

Glu Glu Glu Arg Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg
260 265 270

Glu Met Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg
275 280 285

Met Gly Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly
290 295 300

Gly Ala Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe
305 310 315 320

Pro Pro Leu Gly Gly Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly
325 330 335

Val Pro Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg
340 345 350

Thr Glu Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly
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Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
 35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
 50 55 60
 Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
 65 70 75 80
 Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
 85 90 95
 Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
 100 105 110
 Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
 115 120 125
 Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
 130 135 140
 Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
 145 150 155 160
 Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
 165 170 175
 Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
 180 185 190
 Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
 195 200 205
 Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
 210 215 220
 Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
 225 230 235 240
 Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Cys
 245 250 255
 Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
 260 265 270
 Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
 275 280 285
 Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
 290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly

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Arg	Ala	Met 595	Glu	Gly	Gln	His	Asn 600	Tyr	Leu	Cys	Ala	Gly 605	Arg	Asn	Asp				
Cys	Ile 610	Val	Asp	Lys	Ile	Arg 615	Arg	Lys	Asn	Cys	Pro 620	Ala	Cys	Arg	Leu				
Arg 625	Lys	Cys	Cys	Gln	Ala 630	Gly	Met	Val	Leu	Gly 635	Gly	Arg	Lys	Phe	Lys 640				
Lys	Phe	Asn	Lys	Val 645	Arg	Val	Val	Arg	Ala 650	Leu	Asp	Ala	Val	Ala 655	Leu				
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Phe	Thr	Phe 675	Ser	Pro	Gly	Gln	Asp 680	Ile	Gln	Leu	Ile	Pro 685	Pro	Leu	Ile				
Asn	Leu 690	Leu	Met	Ser	Ile	Glu 695	Pro	Asp	Val	Ile	Tyr 700	Ala	Gly	His	Asp				
Asn 705	Thr	Lys	Pro	Asp	Thr 710	Ser	Ser	Ser	Leu	Leu 715	Thr	Ser	Leu	Asn	Gln 720				
Leu	Gly	Glu	Arg	Gln 725	Leu	Leu	Ser	Val	Val 730	Lys	Trp	Ser	Lys	Ser 735	Leu				
Pro	Gly	Phe	Arg 740	Asn	Leu	His	Ile	Asp 745	Asp	Gln	Ile	Thr	Leu 750	Ile	Gln				
Tyr	Ser	Trp 755	Met	Ser	Leu	Met	Val 760	Phe	Gly	Leu	Gly	Trp 765	Arg	Ser	Tyr				
Lys	His 770	Val	Ser	Gly	Gln	Met 775	Leu	Tyr	Phe	Ala	Pro 780	Asp	Leu	Ile	Leu				
Asn 785	Glu	Gln	Arg	Met	Lys 790	Glu	Ser	Ser	Phe	Tyr 795	Ser	Leu	Cys	Leu	Thr 800				
Met	Trp	Gln	Ile	Pro 805	Gln	Glu	Phe	Val	Lys 810	Leu	Gln	Val	Ser	Gln 815	Glu				
Glu	Phe	Leu	Cys 820	Met	Lys	Val	Leu	Leu 825	Leu	Leu	Asn	Thr	Ile 830	Pro	Leu				

Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr
835 840 845

Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val
850 855 860

Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu
865 870 875 880

His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile
885 890 895

Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val
900 905 910

Ile Ala Ala Gln Leu Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu
915 920 925

Leu Phe His Lys Lys
930

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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
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Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
 100 105 110
 Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
 115 120 125
 Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
 130 135 140
 Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
 145 150 155 160
 Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
 165 170 175
 Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
 180 185 190
 Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
 195 200 205
 Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
 210 215 220
 Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
 225 230 235 240
 Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
 245 250 255
 Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
 260 265 270
 Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
 275 280 285
 Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
 290 295 300
 His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
 305 310 315 320
 Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
 325 330 335
 Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
 340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
 355 360 365
 Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
 370 375 380
 Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
 385 390 395 400
 Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
 405 410 415
 Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
 420 425 430
 Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
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 Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460
 Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480
 Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
 485 490 495
 Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
 500 505 510
 Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
 515 520 525
 Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
 530 535 540
 Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
 545 550 555 560
 Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
 565 570 575
 Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
 580 585 590
 Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
 595 600 605
 Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu

610					615					620					
Arg 625	Lys	Cys	Cys	Gln	Ala 630	Gly	Met	Val	Leu	Gly 635	Gly	Phe	Arg	Asn	Leu 640
His	Ile	Asp	Asp	Gln 645	Ile	Thr	Leu	Ile	Gln 650	Tyr	Ser	Trp	Met	Ser 655	Leu
Met	Val	Phe	Gly 660	Leu	Gly	Trp	Arg	Ser 665	Tyr	Lys	His	Val	Ser 670	Gly	Gln
Met	Leu	Tyr 675	Phe	Ala	Pro	Asp	Leu 680	Ile	Leu	Asn	Glu	Gln 685	Arg	Met	Lys
Glu 690	Ser	Ser	Phe	Tyr	Ser	Leu 695	Cys	Leu	Thr	Met	Trp 700	Gln	Ile	Pro	Gln
Glu 705	Phe	Val	Lys	Leu	Gln 710	Val	Ser	Gln	Glu	Glu 715	Phe	Leu	Cys	Met	Lys 720
Val	Leu	Leu	Leu	Leu 725	Asn	Thr	Ile	Pro	Leu 730	Glu	Gly	Leu	Arg	Ser 735	Gln
Thr	Gln	Phe	Glu 740	Glu	Met	Arg	Ser	Ser 745	Tyr	Ile	Arg	Glu	Leu 750	Ile	Lys
Ala	Ile	Gly 755	Leu	Arg	Gln	Lys	Gly 760	Val	Val	Ser	Ser	Ser 765	Gln	Arg	Phe
Tyr	Gln 770	Leu	Thr	Lys	Leu	Leu 775	Asp	Asn	Leu	His	Asp 780	Leu	Val	Lys	Gln
Leu 785	His	Leu	Tyr	Cys	Leu 790	Asn	Thr	Phe	Ile	Gln 795	Ser	Arg	Ala	Leu	Ser 800
Val	Glu	Phe	Pro	Glu 805	Met	Met	Ser	Glu	Val 810	Ile	Ala	Ala	Gln	Leu 815	Pro
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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
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Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
 260 265 270
 Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
 275 280 285
 Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
 290 295 300
 His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
 305 310 315 320
 Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
 325 330 335
 Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
 340 345 350
 Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
 355 360 365
 Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
 370 375 380
 Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
 385 390 395 400
 Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
 405 410 415
 Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
 420 425 430
 Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
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 Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460
 Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480
 Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
 485 490 495
 Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
 500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625 630 635 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
645 650 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
660 665 670

Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Asp Ser Phe Gly Arg
675 680 685

Ala Thr Lys Ser Asn Pro Val
690 695

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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
 290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
 305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
 325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
 340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
 355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
 370 375 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
 385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
 405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
 420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
 435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
 485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
 500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
 515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
 530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Arg Lys Phe Lys Lys Phe Asn Lys Val Arg Val
595 600 605

Val Arg Ala Leu Asp Ala Val Ala Leu Pro Gln Pro Val Gly Val Pro
610 615 620

Asn Glu Ser Gln Ala Leu Ser Gln Arg Phe Thr Phe Ser Pro Gly Gln
625 630 635 640

Asp Ile Gln Leu Ile Pro Pro Leu Ile Asn Leu Leu Met Ser Ile Glu
645 650 655

Pro Asp Val Ile Tyr Ala Gly His Asp Asn Thr Lys Pro Asp Thr Ser
660 665 670

Ser Ser Leu Leu Thr Ser Leu Asn Gln Leu Gly Glu Arg Gln Leu Leu
675 680 685

Ser Val Val Lys Trp Ser Lys Ser Leu Pro Gly Phe Arg Asn Leu His
690 695 700

Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu Met
705 710 715 720

Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln Met
725 730 735

Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Ser His Arg Ser Leu
740 745 750

Ser Ser Phe Lys Leu Ala Lys Lys Ser Ser Ser Val
755 760

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<213> Homo sapiens

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<309> 2004-09-03

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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
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Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val

245										250					255				
Pro	Pro	Gly	Ala 260	Ala	Ala	Gly	Gly	Val 265	Ala	Leu	Val	Pro	Lys 270	Glu	Asp				
Ser	Arg	Phe 275	Ser	Ala	Pro	Arg	Val 280	Ala	Leu	Val	Glu	Gln 285	Asp	Ala	Pro				
Met	Ala 290	Pro	Gly	Arg	Ser	Pro 295	Leu	Ala	Thr	Thr	Val 300	Met	Asp	Phe	Ile				
His 305	Val	Pro	Ile	Leu	Pro 310	Leu	Asn	His	Ala	Leu 315	Leu	Ala	Ala	Arg	Thr 320				
Arg	Gln	Leu	Leu	Glu 325	Asp	Glu	Ser	Tyr	Asp 330	Gly	Gly	Ala	Gly	Ala 335	Ala				
Ser	Ala	Phe	Ala 340	Pro	Pro	Arg	Ser	Ser 345	Pro	Cys	Ala	Ser	Ser 350	Thr	Pro				
Val	Ala	Val 355	Gly	Asp	Phe	Pro	Asp 360	Cys	Ala	Tyr	Pro	Pro 365	Asp	Ala	Glu				
Pro	Lys 370	Asp	Asp	Ala	Tyr	Pro 375	Leu	Tyr	Ser	Asp	Phe 380	Gln	Pro	Pro	Ala				
Leu 385	Lys	Ile	Lys	Glu	Glu 390	Glu	Glu	Gly	Ala	Glu 395	Ala	Ser	Ala	Arg	Ser 400				
Pro	Arg	Ser	Tyr	Leu 405	Val	Ala	Gly	Ala	Asn 410	Pro	Ala	Ala	Phe	Pro 415	Asp				
Phe	Pro	Leu	Gly 420	Pro	Pro	Pro	Pro	Leu 425	Pro	Pro	Arg	Ala	Thr 430	Pro	Ser				
Arg	Pro	Gly 435	Glu	Ala	Ala	Val	Thr 440	Ala	Ala	Pro	Ala	Ser 445	Ala	Ser	Val				
Ser	Ser 450	Ala	Ser	Ser	Ser	Gly 455	Ser	Thr	Leu	Glu	Cys 460	Ile	Leu	Tyr	Lys				
Ala 465	Glu	Gly	Ala	Pro	Pro 470	Gln	Gln	Gly	Pro	Phe 475	Ala	Pro	Pro	Pro	Cys 480				
Lys	Ala	Pro	Gly	Ala 485	Ser	Gly	Cys	Leu	Leu 490	Pro	Arg	Asp	Gly	Leu 495	Pro				
Ser	Thr	Ser	Ala 500	Ser	Ala	Ala	Ala	Ala 505	Gly	Ala	Ala	Pro	Ala 510	Leu	Tyr				

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625 630 635 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
645 650 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
660 665 670

Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Ser Ile Val
675 680 685

Thr Ser
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<309> 2004-09-03
<313> (1)..(803)

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 35 40 45
 Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
 50 55 60
 Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
 65 70 75 80
 Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
 85 90 95
 Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
 100 105 110
 Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
 115 120 125
 Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
 130 135 140
 Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
 145 150 155 160
 Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
 165 170 175
 Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
 180 185 190
 Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
 195 200 205
 Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
 210 215 220
 Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
 225 230 235 240
 Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
 245 250 255
 Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
 260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr

530					535					540					
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Ser	Leu	Pro	Gln	Lys 565	Ile	Cys	Leu	Ile	Cys 570	Gly	Asp	Glu	Ala	Ser 575	Gly
Cys	His	Tyr	Gly 580	Val	Leu	Thr	Cys	Gly 585	Ser	Cys	Lys	Val	Phe 590	Phe	Lys
Arg	Ala	Met 595	Glu	Gly	Gln	His	Asn 600	Tyr	Leu	Cys	Ala	Gly 605	Arg	Asn	Asp
Cys	Ile 610	Val	Asp	Lys	Ile	Arg 615	Arg	Lys	Asn	Cys	Pro 620	Ala	Cys	Arg	Leu
Arg 625	Lys	Cys	Cys	Gln	Ala 630	Gly	Met	Val	Leu	Gly 635	Gly	Arg	Lys	Phe	Lys 640
Lys	Phe	Asn	Lys	Val 645	Arg	Val	Val	Arg	Ala 650	Leu	Asp	Ala	Val	Ala 655	Leu
Pro	Gln	Pro	Val 660	Gly	Val	Pro	Asn	Glu 665	Ser	Gln	Ala	Leu	Ser 670	Gln	Arg
Phe	Thr	Phe 675	Ser	Pro	Gly	Gln	Asp 680	Ile	Gln	Leu	Ile	Pro 685	Pro	Leu	Ile
Asn 690	Leu	Leu	Met	Ser	Ile	Glu 695	Pro	Asp	Val	Ile	Tyr 700	Ala	Gly	His	Asp
Asn 705	Thr	Lys	Pro	Asp	Thr 710	Ser	Ser	Ser	Leu	Leu 715	Thr	Ser	Leu	Asn	Gln 720
Leu	Gly	Glu	Arg	Gln 725	Leu	Leu	Ser	Val	Val 730	Lys	Trp	Ser	Lys	Ser 735	Leu
Pro	Gly	Phe	Arg 740	Asn	Leu	His	Ile	Asp 745	Asp	Gln	Ile	Thr	Leu 750	Ile	Gln
Tyr	Ser	Trp 755	Met	Ser	Leu	Met	Val 760	Phe	Gly	Leu	Gly	Trp 765	Arg	Ser	Tyr
Lys 770	His	Val	Ser	Gly	Gln 775	Met	Leu	Tyr	Phe	Ala	Pro 780	Asp	Leu	Ile	Leu
Asn 785	Glu	Ser	His	Arg	Ser 790	Leu	Ser	Ser	Phe	Lys 795	Leu	Ala	Lys	Lys	Ser 800

Ser Ser Val

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Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala Arg
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<309> 2004-08-24
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His Arg Arg Gly Gly Gly Gly Gly Arg Gly Gly Leu His Asp Phe Arg
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Ser Pro Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly
35 40 45

Pro Gly Pro Gly Gly Pro Lys Pro Pro Leu Pro Pro Pro Pro His
50 55 60

Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln Gln Pro
65 70 75 80

Pro Pro His Gln Gln Pro Pro Pro His Gln Pro Pro His Gln Gln Pro
85 90 95

Pro Pro Pro Pro Gln Glu Ser Lys Pro Val Val Pro Gln Gly Pro Gly
100 105 110

Ser Ala Pro Gly Val Ser Ser Ala Pro Pro Pro Ala Val Ser Ala Pro
115 120 125

Pro Ala Asn Pro Pro Thr Thr Gly Ala Pro Pro Gly Pro Gly Pro Thr
130 135 140

Pro Thr Pro Pro Pro Ala Val Pro Ser Thr Ala Pro Gly Pro Pro Pro
145 150 155 160

Pro Ser Thr Pro Ser Ser Gly Val Ser Thr Thr Pro Pro Gln Thr Gly
165 170 175

Gly Pro Pro Pro Pro Pro Ala Gly Gly Ala Gly Pro Gly Pro Lys Pro
180 185 190

Gly Pro Gly Pro Gly Gly Pro Lys Gly Gly Lys Met Pro Gly Gly Pro
195 200 205

Lys Pro Gly Gly Gly Pro Gly Met Gly Ala Pro Gly Gly His Pro Lys
210 215 220

Pro Pro His Arg Gly Gly Gly Glu Pro Arg Gly Gly Arg Gln His His
225 230 235 240

Ala Pro Tyr His Gln Gln His His Gln Gly Pro Pro Pro Gly Gly Pro
 245 250 255
 Gly Pro Arg Thr Glu Glu Lys Ile Ser Asp Ser Glu Gly Phe Lys Ala
 260 265 270
 Asn Leu Ser Leu Leu Arg Arg Pro Gly Glu Lys Thr Tyr Thr Gln Arg
 275 280 285
 Cys Arg Leu Phe Val Gly Asn Leu Pro Ala Asp Ile Thr Glu Asp Glu
 290 295 300
 Phe Lys Arg Leu Phe Ala Lys Tyr Gly Glu Pro Gly Glu Val Phe Ile
 305 310 315 320
 Asn Lys Gly Lys Gly Phe Gly Phe Ile Lys Leu Glu Ser Arg Ala Leu
 325 330 335
 Ala Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly Arg
 340 345 350
 Gln Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val Arg
 355 360 365
 Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser
 370 375 380
 Gln Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly
 385 390 395 400
 Arg Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala
 405 410 415
 Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr Thr
 420 425 430
 Thr Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp Glu
 435 440 445
 Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln Lys
 450 455 460
 Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu Tyr
 465 470 475 480
 Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln Gln
 485 490 495

Arg Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu Glu
500 505 510

Ser Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu Arg
515 520 525

Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu
530 535 540

His Ser Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln Glu
545 550 555 560

Glu Glu Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg Glu
565 570 575

Met Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg Met
580 585 590

Gly Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly Gly
595 600 605

Thr Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro
610 615 620

Pro Leu Gly Gly Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly Val
625 630 635 640

Pro Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg Thr
645 650 655

Glu Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly Pro
660 665 670

Arg Gly Met Gly Pro Gly Thr Pro Ala Gly Tyr Gly Arg Gly Arg Glu
675 680 685

Glu Tyr Glu Gly Pro Asn Lys Lys Pro Arg Phe
690 695

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Val Arg Met Ile Asp Val Gly
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Sequence Listing

SEQ ID NO. 1

5 PSF Long Form PSF-A

P23246

707 aa linear

10 Splicing factor, proline-and glutamine-rich (Polypyrimidine tract-binding protein-associated splicing factor) (PTB-associated splicing factor) (PSF) (DNA-binding p52/p100 complex, 100 kDa subunit).

NP_005057

15 splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens].

CAA50283

707 aa linear

20 PTB-associated splicing factor [Homo sapiens].

1 msrdfrfrerg gggggfhrerg ggggrggldh frspppgmg1 nqnrpgmrgg pgqsgpkppi
61 ppppphqqqq qpppqpppq qppphqppph ppphqqqqpp pppqdsskp vaggpgpapg
121 vgsappasss appatppts gpgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
181 agggppppaa vpgpgpgpkq gpgpgpgkkg kmpggpkpgg gpglstpggh pkpphrggge
25 241 prggrqhhipp yhqqhggpp gpgpggrsee kisdsegfka nlsllrpgge ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle srалаeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiers vvivddrgs tgkgivefas
421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpm qkeretpprf
481 aqhgtfeyey sqrwksldem ekqgreveq nmkdakdkle semedayheh qanllrqdlm
541 rrqeelrme elhnqemqkr kemqlrqqee rrrreeemmi rgreemeeqmr rgreesyarm
30 601 gymdprerdm rmgggggamm gdpygsggqk fpplgggggi gyeangpvpp atmssgmmgs
661 dmrterfgqg gagpvggqgp rgmgpgtpag ygrgreeyeg pnkkprf

35 SEQ ID NO. 2

AAH51192

707 aa linear

40 Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens].

1 msrdfrfrerg gggggfhrerg ggggrggldh frspppgmg1 nqnrpgmrgg pgqsgpkppi
61 ppppphqqqq qpppqpppq qppphqppph ppphqqqqpp pppqdsskp vaggpgpapg
121 vgstppasss appatppts gpgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
45 181 agggppppaa vpgpgpgpkq gpgpgpgkkg kmpggpkpgg gpglstpggh pkpphrggge
241 prggrqhhipp yhqqhggpp gpgpggrsee kisdsegfka nlsllrpgge ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle srалаeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiers vvivddrgs tgkgivefas
421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpm qkeretptrf
50 481 aqhgtfeyey sqrwksldem ekqgreveq nmkdakdkle semedayheh qanllrqdlm
541 rrqeelrme elhnqemqkr kemqlrqqee rrrreeemmi rgreemeeqmr rgreesyarm
601 gymdprerdm rmgggggamm gdpygsggqk fpplgggggi gyeangpvpp atmssgmmgs
661 dmrterfgqg gagpvggqgp rgmgpgtpag ygrgreeyeg pnkkprf

55

SEQ ID NO. 3

Isoform short - PSF-F
669aa

5
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61 ppppphqqqq qpppqpppq qppphqppph ppphqqqqpp pppqdsskp vaqsggpapg
121 vgsappasss appatppts appsgsgpgt ptpppavtsa ppgappptpp ssgvpttppq
181 agggppppaa vpgpggpkq gpgpggpkgg kmpggpkpgg gpglstpggh pkpphrggge
10 241 prggrqhhipp yhqhhqggp pggpggrsee kisdsegfka nlsllrpg ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgs tgkgivefas
421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpm qkeretpprf
481 aqhtgfeyey sqrwksldem ekqreqvek nmkdakdkle semedayheh qanllrqdlm
15 541 rrqeelrrme elhnqemqkr kemqlrqqe rrrreemmi rgreemegmr rgreesysrm
601 gymdprerdm rmggggamnm gdpysgggk fpplgggggi gyeangpvpv atmssgmms
661 dmvrmidvg

20 SEQ ID NO. 4

AAH04534
634 aa linear
SFPQ protein [Homo sapiens].

25
1 pqqppppqpp phqppphqp hqqqqppppp qdsskpvaq gpgpapgvg appasssapp
61 atpptsagapp gsgpgptptp ppavtsappg appptppssg vpttppqagg pppppaavpg
121 pggpgkqpgg pggpggkmp ggpkgggpg lstpgghpkp phrgggeprg grqhhyh
181 qhhqggpppg pgggrseekis dsegfkanls llrrpgekty tqrcrlfvgn lpaditedef
30 241 krlfakygep gevfkngkg fgfiklesra laeiakaeld dtpmrgrqlr vrfathaaal
301 svrnlsppys nelleaafsq fgpiervvi vddrgrstgk givefaskpa arkafercse
361 gvfltttpr pvivepleql ddedglpekl agknpmqke retpprfah gtfeeyesqr
421 wksldemkq qreqveknmk dakdklesem edayhehqan llrqdlmrrg eelrrmeelh
481 nqemqkrkem qlrqqeerrr reeemmirqr emeeqmrqr eesysrmgym dprerdmrmg
35 541 gggamnmgdp ysggggkfp lgggggigye anpgvppatm sgsmmsdmr terfgggag
601 pvggqgprgm gpgtpagygr greeyegpnk kprf

40 SEQ ID NO. 5

AAH27708
525 aa linear
SFPQ protein [Homo sapiens].

45
1 msrdfrfrsrg gggggfhrrg ggggrggldh frspppgmg1 nqnrpgmpgp pgqsgpkppi
61 ppppphqqqq qpppqpppq qppphqppph ppphqqqqpp pppqdsskp vaqsggpapg
121 vgsappasss appatppts appsgsgpgt ptpppavtsa ppgappptpp ssgvpttppq
181 agggppppaa vpgpggpkq gpgpggpkgg kmpggpkpgg gpglstpggh pkpphrggge
50 241 prggrqhhipp yhqhhqggp pggpggrsee kisdsegfka nlsllrpg ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgs tgkgivefas
421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpm qkeretpprf
481 aqhtgfeyey sqrwksldem ekqreqvek nmkdakdkl kkkkk

55

SEQ ID. NO. 6

CAA34747

396 aa linear

5 DEFINITION myoblast antigen 24.1D5 (Homo sapiens).

1 efkrlfakyg epgevfkng kgfgfikles ralaaiakae lddtpmrgrq lrvrfathaa
61 alsvrnlspy vsnelleeaf sqfgpierav vivddrgret gkgivefask paarkaferc
121 segvfltttt prpviveple qlddedglpe klaqknpmyq keretpprfa qhgtfeyey
10 181 qrwksldeme kqgrevekn mkdakdkles emedayhehq anlirgdlmr rgeelrrmee
241 lhnqemqkrk emqlrgeeer rrreeemmir qremeeqmr qreesysrmg ymdprerdmr
301 mggggamnmg dpygggqkf pplggggig yeangvppa tmsgsmmgsd mrterfgggg
361 agpvgggqpr gmppgtpagy grgreeyegp nkkprf

15

SEQ ID NO. 7

NM_005066

3071 bp mRNA linear

20 Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA.

X70944 S56626

3071 bp mRNA linear

25 H.sapiens mRNA for PTB-associated splicing factor.

1 ccgccatttt gtgagaagca aggtggcctc cacgtttcct gagegtcttc ttegettttg
61 cctcgaccgc cccttgacca cagacatgtc tcgggatcgg ttccggagtc gtggcggtgg
121 cgggtggtggc ttccacaggc gtggaggagg cggcgccgcg ggcggcctcc acgacttccg
30 181 ttctccgccg ccggcatgg gctcaatca gaatcgccgc cccatgggtc ctggcccggg
241 ccagagcggc cctaagcctc cgatcccgcc accgcctcca caccaacagc agcaacagcc
301 accaccgcag cagccaccgc cgcagcagcc gccaccgcag cagccgcgcg cgcatccaca
361 gccgcatcag cagcagcagc cgcgcgccacc gccgcaggac tcttccaagc ccgtcggtgc
421 tcagggaccc ggcccgcctc ccggagtagg cagcgacca ccagcctcca gctcggcccc
35 481 gcccgcact ccaccaacct cgggggcccc gccagggtcc gggccaggcc cgactccgac
541 cccgcgcctc gcagtcacct cggccccctc cggggcgccg ccacccaccc cgccaagcag
601 cgggggtccct accacacctc ctacggcccg agggcccgcc cctccgcccg cggcagtcoc
661 gggccccgggt ccagggccta agcaggggccc aggtccgggt ggtcccaaaag gcggcaaaat
721 gcctggcggg ccgaagccag gtggcgggccc gggcctaagt acgcctggcg gccaccccaa
40 781 gccgcgcgat cgaggcgggc gggagccccg cgggggcccg cagcaccacc cgccctacca
841 ccagcagcat caccaggggc ccccgcccgg cggggcccgc ggcgcgagcg aggagaagat
901 ctgggactcg gaggggttta aagccaatct gtctctcttg aggaggcctg gagagaaaac
961 ttacacacag cgatgtcggg tggttggtgg gaactctact gctgatatca cggaggatga
1021 attcaaaaaga ctatttgcta aatatggaga accaggagaa gtttttatca acaaaggcaa
45 1081 aggatccgga tttattaagc ttgaatctag agctttggct gaaattgcca aagccgaact
1141 ggatgataca cccatgagag gtagacagct tcgagttcgc tttgccacac atgctgctgc
1201 cctttctgtt cgtaatcttt caccttatgt ttccaatgaa ctggtggaag aagcctttag
1261 ccaatttggt cctattgaaa gggctgttgt aatagtggat gatcgtggaa gatctacagg
1321 gaaaggcatt gttgaatttg cttctaagcc agcagcaaga aaggcatttg aacgatgcag
50 1381 tgaaggtggt ttcttactga cgacaactcc tcgtccagtc attgtggaac cacttgaaca
1441 actagatgat gaagatgggt ttcttgaaaa acttgcccag aagaatccaa tgtatcaaaa
1501 ggagagagaa acccctctc gttttgcccc gcatggcacg tttgagtacg aatattctca
1561 gcgatggaag tctttggatg aaatggaaaa acagcaaagg gaacaagttg aaaaaaacat
1621 gaaagatgca aaagacaaat tggaaagtga aatggaagat gcctatcatg aacatcaggc
55 1681 aaatcttttg cgccaagatc tgatgagacg acaggaagaa ttaagacgca tgggaagaact

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1741 tcacaatcaa gaaatgcaga aacgtaaaga aatgcaattg aggcaagagg aggaacgcag
1801 tagaagagag gaagagatga tgattcgtca acgtgagatg gaagaacaaa tgaggcgcca
1861 aagagaggaa agttacagcc gaatgggcta catggatcca cgggaaagag acatgcgaat
1921 ggggtggcga ggagcaatga acatgggaga tccctatggg tcaggaggcc agaaatttcc
5 1981 acctctagga ggtgggtgtg gcatagggtt tgaagctaatt cctggcggtc caccagcaac
2041 catgagtggg tccatgatgg gaagtgcacat gcgtactgag cgctttgggc agggagggtg
2101 ggggcctgtg ggtggacagg gtcctagagg aatggggcct ggaactccag caggatatgg
2161 tagagggaga gaagagtacg aaggcccaaa caaaaaaccc cgattttaga tggatattt
2221 aggccttcat tccagtttgt tttgtttttt tgtttagata ccaatctttt aaattcttgc
10 2281 attttagtaa gaaagctatc tttttatgga tgttagcagt ttattgacct aatatttgta
2341 aatgggtctg ttgggcaggt aaaattatgt aatgcagtgt ttggaacagg agaatttttt
2401 tttccttttt atttctttat ttttcttttt ttactgtata atgtccctca agtttatggc
2461 agtgtacctt gtgccactga atttccaaag tgtaccaatt tttttttttt tactgtgctt
2521 caaataaata gaaaaatagt tataatattg gatcttcaac tttgccattc atgcttctat
15 2581 gcatattagg ctacgtattc cacattgaaa gcatgagagt gtctaggcct ttgaatggca
2641 tatgccattt ctgggaaatg catctggagg ctaagtattg ctttctacaa ataattgccc
2701 cctttgtttt aaaaagaaga aatgcataat gaagtagttt gatgatttgt ttggcatata
2761 ggaagcacgc tgggtgctaag tattttttaa atggttatgt aagcaaagct gaactgtaaa
2821 tcttcaggaa tatgtattaa gatttgggaa tgggtgtaag acaattggta gggggtgaaa
20 2881 gtgggttga ttaaattgat cttttatggc cctatgatct atcctttact tgaaagcttt
2941 tgaaaagtgg aaaggctatt ttgttgcat tccccatttc ttgtttttta aagaccaaca
3001 aatctcaagc cctataaatg gcttgatttg aacttttaca tttgaattaa agatgttaaa
3061 catgaaaaaa a

25
SEQ ID NO. 8

BC051192
2622 bp mRNA linear
30 Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract
binding protein associated), mRNA (cDNA clone), complete cds.

1 tctgtgtcat ccgccatttt gtgagaagca aggtggcctc cacgtttcct gagcgtcttc
61 ttgcgttttg cctcgaccgc cccttgacca cagacatgtc tcgggatcgg ttccggagtc
35 121 ttggcggtgg cgggtgggtg ttccacaggg gtggaggagg cggcgccgcg ggcggcctcc
181 acgacttccg ttctccgccc cccggcatgg gctcaatca gaatcgcgcc cccatgggtc
241 ctggcccggg ccagagcggc cctaagcctc cgatcccgcc accgcctcca caccaacagc
301 agcaacagcc accaccgcag cagccaccgc cgcagcagcc gccaccgcat cagccgcgcg
361 cgcattccaca gccgcatcag cagcagcagc cgcgcgccac gccgcaggac tcttccaagc
40 421 ccgtcgttgc tcagggaccc ggcccgcctc ccggagtagg cagcacacca ccagcctcca
481 gctcggccccc gcccgccact ccaccaacct cgggggcccc gccagggtcc gggccaggcc
541 cgaactccgac cccgcgcgct gcagtcaact cggccctccc cggggcgccg ccaccacccc
601 cgccaagcag cgggggtccct accacacctc ctccaggcgg agggccgcgc cctccgcccc
661 cggcagtcctc gggcccggtt ccagggccta agcaggggccc aggtccgggt ggtcccaaa
45 721 gcggcaaaat gcctggcggg ccgaagccag gtggcgggcc gggcctaagt acgcctggcg
781 gccaccccaa gccgcgcgct cgaggcgggc gggagccccg cgggggcgcg cagcaccacc
841 cgccctacca ccagcagcat caccaggggc ccccgcccgg cgggcccggc ggcgcgagcg
901 aggagaagat ctccgactcg gaggggttta aagccaattt gtctctcttg aggaggcctg
961 gagagaaaac ttacacacag cgatgtcggt tgtttgttgg gaatctacct gctgatatca
50 1021 cggaggatga attcaaaaga ctatttgcta aatatggaga accaggagaa gtttttatca
1081 acaaaaggcaa aggatctgga tttattaagc ttgaatctag agctttgggt gaaattgcca
1141 aagccgaact ggatgataca cccatgagag gtagacagct tcgagttcgc ttgcccacac
1201 atgctgctgc cctttctgtt cgtaatcttt caccttatgt ttccaatgaa ctgttggaag
1261 aagccttttag ccaatttggg cctattgaaa gggctgttgt aatagtggat gatcgtggaa
55 1321 gatctacagg gaaaggcatt gttgaatttg cttctaagcc agcagcaaga aaggcatttg

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1381 aacgatgcag tgaaggtgtt ttcttactga cgacaactcc tcgtccagtc attgtggaac
1441 cacttgaaca actagatgat gaagatgggtc ttcttgaaaa acttgcccag aagaatccaa
1501 tgtatcaaaa ggagagagaa acccctactc gttttgcccc gcatggcacg tttgagtacg
1561 aatattctca gcatgggaag tctttggatg aaatggaaaa acagcaaaag gaacaagttg
5 1621 aaaaaaacat gaaagatgca aaagacaaat tggaaagtga aatggaagat gcctatcatg
1681 aacatcaggc aaatcttttg cgccaagatc tgatgagacg acaggaagaa ttaagacgca
1741 tggagaact tcacaatcaa gaaatgcaga aacgtaaaga aatgcaattg aggcaagagg
1801 aggaacgacg tagaagagag gaagagatga tgattcgtca acgtgagatg gaagaccaaa
1861 tgaggcgcca aagagaggaa agttacagcc gaatgggcta catggatcca cgggaaagag
10 1921 acatgcgaat ggggtggcga ggagcaatga acatgggaga tccctatggt tcaggaggcc
1981 agaaatttcc acctctagga ggtggtggtg gcataggtta tgaagtaat cctggcggtc
2041 caccagcaac catgagtgtg tccatgatgg gaagtacat gcgtactgag cgctttgggc
2101 agggaggtgc ggggcctgtg ggtggacagg gtcctagagg aatggggcct ggaactccag
2161 caggatatgg tagagggaga gaagagtacg aaggcccaaa caaaaaaccc cgattttaga
15 2221 tgtgatattt aggctttcat tccagtttgt tttgtttttt tgtttagata ccaatctttt
2281 aaattcttgc attttagtaa gaaagctatc tttttatgga tgttagcagt ttattgacct
2341 aatatttcta aatggtctgt ttgggcaggt aaaattatgt aatgcagtgt ttggaacagg
2401 agaatttttt ttcccttttt atttctttat tttttctttt ttactgtata atgtccctca
2461 agtttatggc agtgtacctt gtgccactga atttccaaag tgtaccaatt tttttttttt
20 2521 tactgtgctt caaataaata gaataatagt tataaaaaaa aaaaaaaaaa aaaaaaaaaa
2581 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa

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SEQ ID NO. 9

25

X16850

2021 bp mRNA linear

Human mRNA for myoblast cell surface antigen 24.1D5.

```

30 1 gaattcaaaa gactatttgc taaatatgga gaaccaggag aagtttttat caacaaaggc
61 aaaggattcg gatttattaa gcttgaatct agagcttttg ctgaaattgc caaagccgaa
121 ctggatgata ccccatgag aggtagacag ctctgagttc gctttgccac acatgctgct
181 gccctttctg ttctgtaatct ttcaccttat gtttccaatg aactgttggga agaagccttt
241 agccaatttg gtcctattga aagggtgtgt gtaatagtgg atgacgtggg aagatctaca
35 301 gggaaaaggca ttgttgaaat tgcttctaag ccagcagcaa gaaaggcatt tgaacgtagc
361 agtgaagggtg ttttcttact gacgacaact cctcgtccag tcattgtgga accacttgaa
421 caactagatg atgaagatgg tcttcctgaa aaacttgccc agaagaatcc aatgtatcaa
481 aaggagagag aaacccctcc tcgttttgcc cagcatggca cgtttgagta cgaatattct
541 cagcgatgga agtctttgga tgaatggaa aaacagcaaa gggaaacaagt tgaaaaaac
40 601 atgaaagatg caaaagacaa attggaaagt gaaatggaag atgcctatca tgaacatcag
661 gcaaatcttt tgcgccaaga tctgatgaga cgacaggaag aattaagacg catggaagaa
721 cttcacaatc aagaaatgca gaaacgtaaa gaaatgcaat tgaggcaaga ggaggaaacga
781 cgtagaagag aggaagagat gatgattcgt caacgtgaga tggagaacaa aatgaggcgc
841 caaagagagg aaagttacag ccgaatgggc tacatggatc cacgggaag agacatgcca
45 901 atgggtggcg gaggagcaat gaacatggga gatccctatg gttcaggagg ccagaaattt
961 ccacctctag gaggtggtgg tggcataggt tatgaagcta atcctggcgt tccaccagca
1021 accatgagtg gttccatgat gggagtgac atgcgtactg agcgctttgg gcaggagagt
1081 gcggggcctg tgggtggaca gggctcctaga ggaatggggc ctggaactcc agcaggatat
1141 ggtagaggga gagaagagta cgaagggcca aacaaaaaac ccgattttta gatgtgatat
50 1201 ttaggctttc attccagttt gttttgtttt tttgtttaga taccaatctt ttaattctt
1261 gcatttttagt aagaaagcta tctttttatg gatgttagca gtttattgac ctaatatattg
1321 taaatggtct gtttgggcag gtaaaattat gtaatgcagt gtttggaaac ggagaatttt
1381 ttttcttttt tatttcttta tttttctttt ttactgtat aatgtccctc aagtttatgg
1441 cagtgtacct tgtgccactg aatttccaaa gtgtaccaat tttttttttt ttactgtgct
55 1501 tcaataaat agaaaaatag ttataatatt gatcttcaac tttgccattc atgcttctat

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1561 gcatattagg ctacgtattc cacattgaaa gcatgagagt gtctaggcct ttgaatggca
 1621 tatgccattt ctgggaaatg catctggagg ctaagtattg ctttctacaa ataattgccc
 1681 cctttgtttt aaaaagaaga aatgcatatt gaagtagttt gatgatttgt ttggcatata
 1741 ggaagcacgc tgggtgctaag tattttttaa atggttatgt aagcaaagct gaactgtaaa
 5 1801 tcttcaggaa tatgtattaa gattgtggaa tgggtgtaag acaattggta gggggtgaaa
 1861 gtgggtttga ttaaattgat cttttatggc cctatgatct atcctttact tgaaagcttt
 1921 tgaaaagtgg aaaggtcatt ttgttgcat tccccatttc ttgtttttaa aagaccaaca
 1981 aatctcaagc cctataaatg gcttgattg aaccgaatt c

10

SEQ ID NO. 10

NP_000917

933 aa linear

15

progesterone receptor [Homo sapiens]

AAS00096

933 aa linear

progesterone receptor [Homo sapiens]

20

AAD01587

933 aa linear

progesterone receptor [Homo sapiens]

25

AAA60081

933 aa linear

progesterone receptor Homo sapiens

P06401

30

933 aa linear

Progesterone receptor (PR).

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
 61 prpcqgqdp dektqdqql sdvegaysra eatrgaggss seppekdsq ldsvaldtlla
 35 121 psgpgsqps ppacvtssw clfgpelped ppaapatqrv lslpm srsgc vgdssgtaa
 181 ahkvlpgrls parqlilpas esphwsgapv kpspqaaave veeedssese esagpllkkgk
 241 pralggaaag ggaaacppga aaggvalvpk edsrfisapr alveqdapma pgrsplatv
 301 mdfi hvpilp lnhallaart rqlledesy ggagaasafa pprtspcass tpvavgd fdp
 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafp d fplg
 40 421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
 481 kapgaagc ll prdglpetsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
 541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
 601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggrkfk kfnkvrvvra ldavalp qpl
 661 gvpnesqals qrftfsgqd iqlipplnl lmsiepdviy aghdntk pdt sssltslnq
 45 721 lgerqlslsv kwskslpgrf nlhiddqitl iqyswmalmv fglgwrsykh vsgqmlyfap
 781 dlilneqrmk essfyslclt mwqipqefvk lqvsqeeflc mkvlllnti pleglrsqtq
 841 feemrssyir elikaiglrq kgvsssqrf yqltklldnl hdlvkqlhly clntfiq sra
 901 lsvefpemms eviaaqlpki lagmvkpllf hkk

50

SEQ ID NO. 11

BAB91074

831 aa linear

55

delta 4 progesterone receptor [Homo sapiens]

```

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgqdps dektqdqqs1 sdvegaysra eatrgaggss ssppekds1g1 lds1vldt1la
121 psgpggsgqs ppacvtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
5 181 ahkvlprgls parqlllpas esphwsgapv kpspgaaave veeedgsese esagp1lk1gk
241 pralggaaag ggaaavppga aaggvalvpk edsrfasprv alveqdapma pgrsplattv
301 mdfi1hvpilp lnhallaart rqlledesy1d ggagaasafa pprsspcass t1pvavgd1fdp
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafp1df1lg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
10 481 kapgasgcl1 prdglp1tsa s1aaaagaapa lypal1g1ng1 pqlgyqaav1 keglp1qv1yp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrn1 hiddqitliq yswmslmvfg
661 lgwrsykhvs gqml1yfapdl ilneqr1mkes sfyslcltmw qipqefvklq vsqeeflcmk
721 vlll1ntipl eglrsqtqfe emrssyirel ikaiglrqkg vvsssqrfyq ltkl1ldn1hd
15 781 lvkq1hlycl ntfigsrals vefpemmsev iaaqlpkila gmvkpl1fhk k

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SEQ ID NO. 12

BAC06585

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20 695 aa linear
Progesterone receptor [Homo sapiens]

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1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgqdps dektqdqqs1 sdvegaysra eatrgaggss ssppekds1g1 lds1vldt1la
25 121 psgpggsgqs ppacvtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspgaaave veeedgsese esagp1lk1gk
241 pralggaaag ggaaavppga aaggvalvpk edsrfasprv alveqdapma pgrsplattv
301 mdfi1hvpilp lnhallaart rqlledesy1d ggagaasafa pprsspcass t1pvavgd1fdp
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafp1df1lg
30 421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcl1 prdglp1tsa s1aaaagaapa lypal1g1ng1 pqlgyqaav1 keglp1qv1yp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrn1 hiddqitliq yswmslmvfg
661 lgwrsykhvs gqml1yfapdl ilndsfgrat kanpv
35

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SEQ ID NO. 13

BAC11011

```

40 764 aa linear
delta 3+6/2 progesterone receptor [Homo sapiens].

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```

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgqdps dektqdqqs1 sdvegaysra eatrgaggss ssppekds1g1 lds1vldt1la
45 121 psgpggsgqs ppacvtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspgaaave veeedgsese esagp1lk1gk
241 pralggaaag ggaaavppga aaggvalvpk edsrfasprv alveqdapma pgrsplattv
301 mdfi1hvpilp lnhallaart rqlledesy1d ggagaasafa pprsspcass t1pvavgd1fdp
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafp1df1lg
50 421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcl1 prdglp1tsa s1aaaagaapa lypal1g1ng1 pqlgyqaav1 keglp1qv1yp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegrkf
601 kkfnkvrvvr aldavalppq vgvpn1esqal sqrftf1spgq diqlip1plin llmsiep1dvi
661 yaghdntkpd tss1l1ts1n qlgerq1llsv vkwsks1pgf rnlhiddqit liqyswms1m
55 721 vfglgwrsyk hvsgqml1yfa pdlilneshr sls1fklakk sssv

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SEQ ID NO.14

5 BAC11012
690 aa linear
delta4+6/2 progesterone receptor [Homo sapiens]

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1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
10 61 prpcqgqgps dektqdqql sdvegaysra eatrgaggss ssppekdsq ldsvidtlla
121 psgpgqsgps ppacvtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrfasprv alveqdapma pgrsplattv
301 mdfihipilp lnhallaart rqlledesy dggagaasafa pprsspcass tpvavgdffpd
15 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdpplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcll prdglpstea saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 yllylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
20 661 lgwrsykhvs ggmlyfapdl ilneqsivts

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SEQ ID NO.15

25 BAC11013
803 aa linear
delta 6/2 progesterone receptor [Homo sapiens].

```

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
30 61 prpcqgqgps dektqdqql sdvegaysra eatrgaggss ssppekdsq ldsvidtlla
121 psgpgqsgps ppacvtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrfasprv alveqdapma pgrsplattv
301 mdfihipilp lnhallaart rqlledesy dggagaasafa pprsspcass tpvavgdffpd
35 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdpplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcll prdglpstea saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 yllylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlgggrfk kfnkvrsvra ldavalpqp
40 661 gvpnesqals qrftfsggqd iqlipplinl lmsiepdviy aghdntkpd ssslltslnq
721 lgerqllevv kwekslpgfr nlhiddqitl iqyswmslmv fglwrsykh veggmlyfap
781 dlilneshrs lssfklakks ssv

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45 SEQ ID NO. 16

FGQGGAGPVGGQGP

50 SEQ ID NO.17

CTGAGTC

55 SEQ ID NO. 18

YGEPEGVFINKGK

5 SEQ ID NO. 19

GIVEFASKPAAR

10 SEQ ID NO. 20

FAQHGTEEYEYSQR

15 SEQ ID NO. 21

NP_076092 (Murine PSF)

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